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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

JOURNAL MEDLINE	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AF034633	RESULT 1
secretagogue and neurocensin receptors Genomics 46 (3), 426-434 (1997) 98110578	Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone	McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Feighner, S.D.,	1 (bases 1 to 1362)	Eukaryota; Metazoa; Chordata; Craniata; Verlebrata; Euceleoscomi; Mammalia: Eutheria: Drimates: Catarrhini: Hominidae; Homo.	Homo sapiens	human.		AF034633.1 GI:2654160	AF034633	complete cds.	Homo sapiens orphan G protein-coupled receptor (GPK39) IIIKNA,	AF034633 1362 bp mRNA PRI 13-00-11996		

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MCKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D.
Hreniuk,D.L., Smith,R.G., Van Der Ploeg,L.H.T. and Howar
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/db_xref="G1:2654161"
/tanslation="MASPSLPGSDCSQIIDHSHVPEEEVATWIKITLILVYLIIFVMG
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VTSALVALPLLFAMGTEYPLVNVPSHRGLTCNRSSTRHHEDPETSNMSICTNLSSRWI
VFOSSIFGAFVVYLVVLLSVAFMCWNMMQVLMKSQKGSLAGGTRPPQLRKSESESRT
ARRQTIIFLRLTVVTLAVCWMENQIRRIMAAARKHDWTRSVFRAYMILLFESSTFFY
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KEYWORDS SOURCE

ORGANISM

Homo sapiens

human

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

Euteleostomi;

ACCESSION DEFINITION

N Homo sapiens chromosome 2 clone SEQUENCE, 22 unordered pieces. AC068744 GI:10567984 HTG; HTGS_PHASE1: HTGS TRAFF

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HTG RP11-666P13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Colloge,S., Domino,M., Doyle,M., Ferreira,P., FitcHugh,W., Gage,D., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitcHugh,W., Gage,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Oct 4, 2000 this sequence version replaced gi:7717151. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 2, clone RP11-666P13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will be preserved.
17735; contig of 17735 bp in length
17736 17835; gap of 100 bp
17836 45012; contig of 27177 bp in length
45013 45112; gap of 100 bp
45113 46230; contig of 1118 bp in length
46231 46330; gap of 100 bp
46331 47605; contig of 1275 bp in length
4706 47705; gap of 100 bp
49343 49442; gap of 100 bp
49343 49442; gap of 100 bp
49443 51470; contig of 1637 bp in length
49443 19442; gap of 100 bp
49443 19442; gap of 100 bp
49443 19442; gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 163890 bases at least Q30 Consensus quality: 169058 bases at least Q30 Consensus quality: 171182 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L9278
Center clone name: 666_P_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 170000; agarose-fp
Insert size: 172394; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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77078 82744: contig of 5667 bp
82745 82844: gap of 100 bp
82845 90681: contig of 7837 bp
90682 90781: gap of 100 bp
90782 98252: contig of 7471 bp
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174224 174323; gap of 170
174324 174494; contig of 171
174324 174494; contig of 171
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107827 107926: gap of
107927 117679: cont
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141000 141099; gap of 100 bp
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53724 53823: gap of 100 bp
53824 56799: contig of 2976 bp in length
56800 56899: gap of 100 bp
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644991 70638: contig of 5648 if
70639 70738: gap of 100 bp
70739 76977: contig of 6239 i
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60203: gap of 100 --
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107826: contig of 9474 bp in length
07926: gap of 100 bp
117679: contig of 9753 bp in length
17779: gap of 100 bp
129303: contig of 1524 bp in length
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ilarity 100.0%; Pred. No. 1.2e-161;
Conservative 0; Mismatches 0;
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Direct Submission
Submitted (09-AUG-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Aug 9, 2001 this sequence version replaced gi:14488388.
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                                                                                                                                                                                                                                                                                                                              /protein_id="CAC39782.1"
/db_xxef="GI:14272688"
/db_xxef="GI:14272688"
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NCTVNYQDMCQKEYMEQSAGIMYRKSCASSAACLIASAGYQSFCSPGKLNSVCISCCN
                                                                                                                                                                                                                                                                                                  PHLPE"
                                                                                                                                                                                                                                                                                                                	ext{TPLCNGPRPKKRGSSASALRPGLRTTILFLKLASSRHTAELKEMPPPPALFFQPSPPT}
                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                    [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.5kb.The Sfil-digested PCR product was cloned into distinct braIII sites of pME185-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Library was constructed by Sugano et al. (University of Tokyo, Institute of CTTCTGCTTAAAACCTGCG); 3' end primer [CGACCTGCAGCTCGAGCACA])
                                                                                                                                                                                                                                                                                                                                      Katsuyuki Hashimoto, National Institute of Infectious Division of Genetic Resources; 23-1, Toyama 1-chome, S Tokyo 162-6640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/
Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
URL: http://www.nih.go.jp/yoken/genebank/
Lib Name: Sugano mouse brain mncb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1797)
Hashimoto,K., Osada,N., Kusuda,J. and Sugano,S.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fis (full insert sequence).
Mus musculus (strain:C57BL) adult female cDNA to mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         made by oligo-capping method
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                                                                                                                                                                                                                                                                 Lab host:
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  part of this sequence
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Location/Qualifiers 1. .1797 /organism="Mus musculus"

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ORIGIN
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SOURCE
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                             REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCAGCCCGCAGCCCCCTCATCTTCCTAGCCTCCCGGCGCAGTAACTCTTCCTCCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTCCTCTCAGCAGTTCCGGAAGGTGTTCTGGCAGGTGCTCTGCTGCCGCCTGACTCTGC
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             Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 587)
Ota,T., Isogai,T., Ni
Ota,T., Is
Hayashi,K.
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                                                                                                                                    Sequence 620
AX136698
                                                                        Homo sapiens
                                                                                         human
                                                                                                                      AX136698.1
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/COGON_STATT=1
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NCTVNVQDMCQKEVFEQSAGAIRPGLLTTLLFFHLALCLAHC"
TPLCNGPRPKKRGSSASAIRPGLLTTLLFFHLALCLAHC"
511 g 408 t
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/db_xref="taxon:10090"
/clone="MNCb-0671"
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/dev_stage="adult"
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                                                                                                                        GI:14273102
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75.0%;
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                  Nishikawa,
                                              Chordata;
Primates;
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Pred. No. 4.2e-47;
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                , T . ,
                                               Catarrhini;
                                                             Craniata; Vertebrata; Euteleostomi;
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                    Kawai,Y.,
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TAKEDA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding human neurotensin
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Homo sapiens (human)
JP 1996143597-A/1
04-JUN-1996
24-NOV-1994 JP 1994289882
ONDA HARUO, OOGI KAZUHIRO, HINUMA KUNIJI, MASUO YOSHINORI
COYKI4/72,A61K38/00,A61K45/00,A61K45/00,A61K45/00,
A61K45/00,
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                      acccgccaccacgagcagcccgagacctccaatatgtccatctgtaccaacctctccagc 645
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                                                                     actgagtaccccctggtgaacgtgcccagccagcggggtctccacttgcaaccgctccagc 585
                                                                                                    ATCAGCGCCATCTGGCTCGCCTCGGCCCTGCTGGCGGTGCCTATGCTGTTCACCATGGGC 624
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/note="Known human neurotensin receptor
protein"
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/cell_line="human colon adenocarcinoma HT-29"
/clone="phNTR84-14"
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                                                                                                                                                                                                                                                                                                                              Cloning and expression of a complementary DNA encoding a high affinity human neurotensin receptor FEBS Lett. 317 (1-2), 139-142 (1993)
                                                                                                                                                                                                                                                                                                                                                                                    Vita, N., Laurent, P., Lefort, S., Chalon, P., Dumont, X., Kaghad, M., Gully, D., Le Fur, G., Ferrara, P. and Caput, D.
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-DEC-1992) N. Vita, Sanofi Elf Bio Recherches, Bp 137, 31676 Laberge Cedex, FRANCE (bases 1 to 4131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4131)
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x70070.1 GI:35020
G-protein coupled receptor; neurotensin receptor.
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Direct Submission
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          /gene="NTRR"
/codon_start=1
/product="neurotensin receptor"
/protein_id="CAA49675.1"
/db_xref="GI:35021"
                                                                                                                    /gene=
                                                                                                                                                        /clone_
                                                                                                                                                                                           /cell_type="adenocarcinome"
/cell_line="HT29"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="SWISS-PROT:P30989"
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                                                                                                    1228 TTCAGCATGGCCATCGAGCCTGGCAGGGTCCAGGCCCTGCGGCACGGCGTGCGCGTCCTA 1287
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856 aggctgattgttgtgacattggccgtatgctggatgcccaaccagattcggaggatcatg 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            967 CTGACGGTGCCTATGCTGTTCACCATGGGCGAGCAGAACCGCAGCGCCGACGGCCAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         847 GTGGCCAGCCTGAGTGTGGAGCCCTACCTGCCATCTGCCACCCCTTCAAGGCCAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 gtgctgacactcagctttgagcgctacatcgccatctgtcaccccttcaggtacaaggct
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                                                                                                                                                                     ctgaggaagtccgagagcgaagagcaggaccgccaggaggcagaccatcatcttcctg 855
                                                                                                                                                                                                                                                                                                                                                                             CCCATGGTGGTCATCTCGGTCCTGAACACCATCATCGCCAACAAGCTGACCGTCATGGTA 1173
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TPFLYDFYHYFYMVTNALFYVSSTINPILYNLVSANFRHIFLATLACLCPVWRRRRKR
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Pred. No. 3.5e-23;
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                                                                                                                                                       Sequence split into 4 fragments LOCUS AL357872 Accession AL357872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                  Fragment Name
AL357872_0
AL357872_1
AL357872_2
                                                                   AL357872_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1528
                                                                                                                                                                                                                                                                   387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1288 CGTGCAGTGGTCATCGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGGCGCCTCATG 1347
                                                                                                                                                                                                                                                                                                                                                      908 ggatcatggctgcggccaaacccaagcacggctggacgaggtcctacttccgggcgtaca 967
                                                                                                                                                                                                                                                                                                                                                                                                          267 TCTGCCCAGGGCTGATTGTTGTGACATTGGCCGTATGCTGGATGCCCAACCAGATTCGGA 326
                                                                                                                                                                                                                                                                                                                                                                                                                               848 tetteetgaaggetgattgttgttgtgacattggeegtatgetggatgeecaaccagattegga 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                TGATCCTCCTCCTTCTCGGAGACGTTTTTCTACCTCAGCTCGG
                                                                                                                                                                                                                                                                                                 tgatcctcctccccttctcggagacgtttttctacctcagctcgg 1012
                                                                                                                                                                                                                                                                                                                                     GGATCATGGCTGCGGCCAAACCCAAGCACGACGACGAGGTCCTACTTCCGGGCGTACA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cagcacgccaaccacgagaagc 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCGTCTCTGCCAACTTCCGCCACATCTTCCTGGCCACACTGGCCTGCCCTGCCCGGTG 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtgtcctcgcagcagtttcggcgggtgttcgtgcaggtgctgtcgtgtgccgcctgtcgctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctccccttctcggagacgtttttctacctcagctcggtcatcaacccgctcctgtacacg 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCGGCGCAGGAGGAAGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACATGGTGACCAACGCACTCTTCTACGTCAGCTCCACCATCAACCCCCATCCTGTACAAC 1467
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           AL357872 367980 bp DNA HTG Homo sapiens chromosome 9 clone RP11-308P9, PROGRESS ***, 55 unordered pieces.
AL357872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Differential gene expression in cancer Patent: WO 0136685-A 95 25-MAY-2001; NYXIS NeuroTherapies, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 444) Kroes,R.A., Moskal,J.R. and Yamamoto,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 95 from Patent W00136685 AX150120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/db_xref="taxon:9606"
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200001
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367980 bp
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Pred. No. 9.3e-22;
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                               SEQUENCING
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 362580; sum-of-contigs
Insert size: 177412; 7.0% error; agarose-fp
Quality coverage: 4.17x in Q20 bases; sum-of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 28, 2000 this sequence version replaced gi:11340280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: bA308P9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Sanger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will be preserved.
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17530 17629: gap of 100 bp
17630 25254: contig of 7625 bp in length
25255 2534: gap of 100 bp
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                                         81130: gap of
90501: cont
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277: gap of 100 bp
33210: contig of 2933 bp in length
                                                                                                                    598: gap of 100 bp
77580: contig of 13882 bp in length
380: gap of 100 bp
81030: contig of 3350 bp in length
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53590: contig of 2155 bp in length
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100 bp
f 9371 bp in length
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313756 31614:
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174378 174477:
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90602 98709: contig of 8108 i
98710 98809: gap of 100 bp
98810 107616: contig of 8807 i
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229357: contig of 3887 bp in
229457: gap of 100 bp
231791: contig of 2334 bp in
231791: contig of 100 bp
                                                        308487:
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               313655: com
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                                                                                 305013: cc.
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                                                                                                                  0554: gap of 100 up
292423: contig of 11869 bp in length
32523: gap of 100 bp
298279: contig of 5756 bp in length
                                           лв487: gap of
311059: conti
                                                                  308387: cont
                                                                                                                                                                              100 bp
280454: contig of 12448 bp in length
                                                                                                                                                                                                                              11481: gap of 100 bp
258412: contig of 16931 bp in length
                                                                                                                                                                                                                                                                                                                                           222979: contig of 2482 by 13079: gap of 100 bp 225370: contig of 2291 bp
                                                                                                                                                                                                                                                                                                                                                                                         76697: gap of 100 bp 220397: contig of 13700 bp
3755: gap of 
316142: contig of
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108°
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144404: contig of 7362
4504: gap of 100 k
158206: contig of 13702
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125: contig of 3442 bp 1

125: contig of 30 bp

125: gap of 100 bp

127: contig of 9372 bp 1

127: gap of 100 bp

128: gap of 100 bp

139: contig of 3994 bp 1
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466 attggcttcgtctgggtcacctccgccctggtggcactgcccttgctgtttgccatgggt 525
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337191 367980: contig of 30790 bp in length
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/chromosome="9"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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                           misc_feature
                                                                                         misc_feature
                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw.; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20

IMPORTANT: This sequence is not the entire insert of clone RP11-93B14 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP11-93B14 is at 1 in this sequence. The true left end of clone RP11-93B14 is at 114543 in this sequence. The true left end of clone RP11-93B14 is at 114543 in this sequence. The chemistry or covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-93B14 is from the library RP1-11 constructed by the groun of pleter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 actgagtacccctggtgaacgtgcccagccaccggggtctcacttgcaaccgctccagc
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On Oct 1, 2000 this sequence version replaced gi:10277960.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human DNA sequence from clone RP11-93B14 on chromosome 20 Contains the SLC21A12 gene for solute carrier family 21 (organic anion transporter) member 12, the 5' end of the NTSR1 gene encoding the high affinity neurotensin receptor 1, a novel gene, 4 CpG islands,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL357033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heath, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                          http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                              For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                             the library RPCI-11.1 constructed by the group of Pieter de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 114642)
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                                                                                                                                                                                                                                                                                               1. .114642
                                                                                                                                                                                            /db_xref="taxon:9606"
/chromosome="20"
/note="match: GSS: Em:AQ312036"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                      /note="Single clone region"
                                                                                                                    /clone_lib="RPCI-11.1"
                                                                                                                                                             /clone="RP11-93B14"
                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/note="match: cDNAs: Em:AB031051

match: ESTS: Em:AI022939 Em:AA280994 Em:AW574753

Em:AI347130 Em:AW027513 Em:AI803717 Em:AA878131"
                                                                                                                                                                                                /note="4 copies 56 mer 96% conserved"
join(20078. .20969,22396. .22486,24131. .24252,24783. .2
28653. .28807,30099. .30294,31464. .31629,31731. .31903,
32196. .32260,32649. .32797,35489. .36012)
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15722. .1
                                                                                                                                                                                                                                                                                                                                                                                                                            17936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17515.
                                                                                                                                                                                         'gene="SLC21A12"
                                                                                                                                                                                                                                                                                                                                                    /note="MLT1B repeat: matches 303. .440 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                  18516.
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1PA5 repeat: matches 5898. .6145 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15932
                                                                                                                                                                                                                                                                                                          'note="MLT1B repeat: matches 1. .181 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                         /note="MLTIC repeat: matches 53. .194 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L2_repeat: matches 2625, .2687 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SLC21A12"
7519. .7748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/product="bA93B14.1.1 (solute carrier family 21 (organic
anion transporter) member 12, isoform 1)"
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5375. 5553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="MIR repeat: matches 29. .138 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="9 copies 4 mer tgtg 83% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MLT2CB repeat: matches 1. .501 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       match: ESTs: Em:AI022939 Em:AI347130 Em:AW574753 Em:AAA80994 Em:AI348176 Em:AA534529 Em:AI803717"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                revidence=not_experimental
join(6239. .6272,20078. .20969,22396. .22486,24131. .242
24783. .24894,28653. .28807,30099. .30294,31464. .32260,
32649. .32797,35469. .36012)
/gene="SLC21A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="6 copies 13 mer 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 8. .246 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="match: cDNAs: Em:AF104334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="CpG island"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: GSS: Em:AZ537553"
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/note="18 copies 2 mer aa 88% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="2 copies 40 mer 93% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .9251
                                                                                                                                                                                                                                                                                                                                                                                .18653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 copies 45 mer 96% conserved" .15816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .15969
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                                                                                                                                                                                                                                                                                                                                         0988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             copies 6 mer caccct 89% conserved"
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                                       .24252,24783. .24894,
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                                        Local Similarity
            274;
            Conservative
                                                                                                                                                                                                                                                                22857. .22956
/note="5 copies 20 mer 70% conserved"
22959. .23010
                                                                                                                   /note="3 copies 46 mer 94% conserved"
                                                                                                                                                                                 /note="2
                                                                                                                                                                                                                                                                                                                                                                                                /note="5 copies 22 mer 72% conserved" 22856. .22959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSAVIKFCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNLTAPCNAAC SCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDGQKVYRDCSCIPQNLSSGFGHAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATACFLYKPLSESSDGLETCLPSQSSAPDSATDSQLQSSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPGSQRYAVMRAAEMHOLKDSSRGEASNPDFGKTIRDLPLSIWLLLKNPTFILLCLAG
ATEATLITCMSTFSPKFLESQFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STSGLSRYOLVFMLGOFLHGVGATPLYTLGVTYLDENVKSSCSDVYIATFYTAAILGP
AAGYLIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFTAVPILGYPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MPLHQLGDKPLTFPSPNSAMENGLDHTPPSRRASPGTPLSPGSLRSAAHSPLDTSKQPLCQLWAEKHGARGTHEVRYVSAGQSVACGWWAFAPPCLQVLNTPKGILFFLCAAAFLQGMTVNGFINTVITSLERRYDLHSYQSGLIASSYDIAACLCLTFVSYFGGSGHKPRWLGWGVLLWGTGSLVFALPHFTAGRVEVELDAGVRTCPANPGAVCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="bA93B14.1.2 (solute carrier family 21 (organic anion transporter) member 12, isoform 2)"
/protein_id="CAC14220.1"
/db_xref="GI:11121399"
                                                                                                                                                                                                                                   /note="26 copies 2 mer ag 73% conserved"
                                                                                                                                                                                                                                                                                                                                                          /note="26 copies 4 mer agag 68% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {	t AGKCTSTCQRKPLLLVFIFVVIFFTFLSSIPALTATLRCVRDPQRSFALGIQWIVVRI}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLPLVIGAIVGLPRCTETVAVSLRIFPLVLAMPLOGNALQLVRESPSFWFSYSL"
join(20174. 2096),22396. 22486,24131. 24252,24783. 28653. 28807,30099. 30294,31464. 31629,31731. 31903
32196. 32260,32649. 32797,35469. 35612)
/gene="SLC21A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="2 copies 75 mer 90% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGIPGPIAFGWVIDKACLLWQDQCGQQGSCLVYQNSAMSRYILIMGLLYKVLGVLFF
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ATEATLITGMSTFSPKFLESQFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGYLIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFTAVPILGYPRO
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SYFGGSGHKPRWLGWGVLLMGTGSLVFALPHFTAGRYEVELDAGVRTCPANPGAVCAD
STSGLSRYQLVFMLGQFLHGVGATPLYTLGVTYLDENVKSSCSPVYIAIFYTAAILGP
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/protein_id="CAC14919.1"
/db_xref="GI:11121398"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="SLC21A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDGQKVSGAAAYRPCPPLDPGKGPP
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                                  11.0%;
                                                                                                                                                        '2 copies 40 mer 92% conserved" .26575
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                                                                                                                                                                                                                    .23601
         0;
                               Score 150.4; DB 9; Length 114642; Pred. No. 1.4e-20;
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   Mismatches
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Direct Submission
Submitted (20-AUG-1998) to the DDBJ/EMBL/GenBank databases. Hideki Submitted (20-AUG-1998) to the DDBJ/EMBL/GenBank data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammālia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus whole brain cDNA to mRNA.
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/db_xref="0:3551525"
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ESILEPNSNLDVNTDIYSKYLNTANVLLALFVVGTTVANVLLASALAVPMLFTMGQNRSADQVA
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RRRKKRPTESRKPNSMSSNHAFSTSATRETLY"
                                                                                                                                                                                                PGGLVCTPFYDTATVKVVIOVNTFMSFLEPMLIISILNTVIANKLTVMVHQAAEQGRG
VCTVGTHNSLEHSTFNMSIEPGRVQALRHGVLVLRAVVIAFVVCWLPYHVRRLMFCYI
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/db_xref="taxon:10090"
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1274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTATTCCAAGGTGCTGGTGACCGCTGTATACCTGGCACTTTTTGTGGTGGGCACTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cctggatcaaaatcacccttattctggtgtaccttgatcatcttcgtgatgggccttctgg 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aggigacagaccacaiggigagittiggcitgcicggacaictiggigiticcicaicggca 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggaacagogocoaccattogggtcaccocaggtgotgcagaagaaaggatacttgcagaagg 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTACCCATGCTTTTCACCATGGGCCTGCAGAACCGCAGTGCCGATGGCCAGCACCCTG 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cactgcccttgctgtttgccatgggtactgagtaccccctggtgaacgtgcccagccacc 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgggaccttgccaggtgaagctgctgattggcttcgtctgggtcacctccgccctggtgg 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGCCTGAGTGTGGAGCGCTACTTGGCCATCTGCCATCCCTTCAAGGCCAAGACCCTCA 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgacactcagctttgagcgctacatcgccatctgtcaccccttcaggtacaaggctgtgt 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCCCGTGGAGCTGTACAACTTCATCTGGGTGCACCATCCCTGGGCCTTTGGGGATGCTG 861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTCCCGCAGCCGCACCAAGAAATTCATCAGTGCCATATGGCTAGCCTCGGCGCTGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggggtctcacttgcaaccgctccagcacccgccaccacgagcagcccgagacctccaata 619
                                                                                                                                                             tgattgttgtgacattggccgtatgctggatgcccaaccagattcggaggatcatggctg 919
                                                                                                                                                                                                             ACATGTCCATCGAGCCAGGCCGTGTCCAGGCCCTGCGCCATGGAGTCCTCGTCTTACGTG 1377
                                                                                                                                                                                                                                                                                 GTGCACCGTGGGCACCCACAACAGTTTAG------AGCACCACCACCACCACCATCA 1317
                                                                                                                                                                                                                                                                                                              aggigotoaigaaaagcoagaagggotogoigggogggggacgoggggctocgcagoiga 799
                                                                                                                                                                                                                                                                                                                                                     CCAACAAACTGACCGTCATGGTGCACCAGGCTGCCGA-----GCAGGGCCGTGGTGT 1273
                                                                                                                                                                                                                                                                                                                                                                           cettegtggtetacetegtggteetgeteteegtageetteatgtgetggaacatgatge 739
                                                                                                                                                                                                                                                                                                                                                                                                                         ACACCTTCATGTCCTTCCTGTTTCCCATGCTGATCATCTCCATCCTAAACACTGTGATAG
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                                                                                                                                                                                                                                            ggaagtoogagagogaagagagagacogocaggaggoagacoatcatottootgaggo 859
                                                                                                                                           CTGTGGTAATCGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGGCGCCTCATGTTCT 1437
                                 cottotoggagacgtttttctacctcagctcggtcatcaacccgctcctgtacacggtgt 1039
                                                                     GCTATATCTCAGATGAACAGTGGACTACGTTCCTCTTCGACTTCTACCACTATTTCTATA 1497
                                                                                                 cggccaaacccaagcacgactggacgaggtcctacttccgggcgtacatgatcctcctcc
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46.8%;
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181 aaaggatacttgcagaaggaggtgacagaccacatggtgagtttggcttgctcggacatc 240
                                                                                                                      807 CCCGAG-TTGAGGTGACCCCACGGTCCAGAATCATCCTCATTCTGGTGAACCTGGTTCTC 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1618 GCCGCCGCCGAAAGAAGAGGC 1638
                                                                                                                                                                                                               747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1558 TCTCCGCCAACTTCCGCCAGGTCTTCCTGTCCACACTGGCTTGCCTCTGTCCTGGGTGGC 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1100 acgccaaccacgagaagcgcc 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1040 cctcgcagcagtttcggcgggtgttcgtgcaggtgctgttgctgccgcctgtcgctgcagc 1099
                                                                                                                                                                       61
                                                                                                                                                                                                                            1 atggcttcacccagcctcccgggcagtgactgctcccaaatcattgatcacagtcatgtc 60
                                                                                                                                                                                                                                                                                                                Local
                                                                     ttcgtgatgggccttctggggaacagcgccaccattcgggtcacccaggtgctgcagaag 180
                                                                                                                                                    cccgagtttgaggtggccacctggatcaaaatcacccttattctggtgtacctgatcatc 120
                                            TTTGTGGTGGGCATACTGGGTAGGAGAATCACCCAAAGGTCACCCATGAGCTGCAGAAAA 925
                                                                                                                                                                                                    ATGGCTTCACCTAGTGGCCCCAAGCATGACTTCTCCCCATGTCAATGAGCACAGCCACGTT 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agency).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
2 (bases 1 to 1239)
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligo capping, fis (full insert sequence). Homo sapiens human small intestine cDNA to mRNA, clone_lib:HSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H.
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                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="human small intestine"
/note="cloning vector pME18SFL3"
240 c 236 g 418 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="HSI00196"
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cDNA: FLJ22542 fis, clone HSI00196.
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                   Score 124.8; DB 9;
Pred. No. 4.3e-15;
0; Mismatches 97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                           Length 1239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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241 ttggtgttcctcatcggcatgcccatggagttctacagcatcatctggaatc 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 1% of reads
Sequencing vector: plasmid; L08752; 98% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 170334 bases at least Q40
Consensus quality: 170496 bases at least Q30
Consensus quality: 170538 bases at least Q20
Insert size: 170595; sum-of-contigs
Insert size: 163233; 4.6% error; agarose-fp
Ouality coverage: 7.58x in Q20 bases; sum-of-contigs Quality
Coverage: 9.52x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown. 
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: bA496H23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 170695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 10 clone RP11-496H23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL391318.20 GI:15131827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                         1 50299: contig of 50299 bp in length 50300 50399: gap of 100 bp 50400 170655: contig of 120296 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
/note-"assembly_fragment:02503"
50400. .170695
/note-"assembly_fragment:04092"
/131970 c 32022 g 54189 t 1
                                                                                                                                                                                                   /db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-496H23"
                                                                                                                                                                                                                                                                                                                                     1. .170695
                                                                                                                                                                       /clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170695 bp
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100 others
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AL157394
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3554 CCCGAG-TTGAGGTGACCCCACGGTCCAGAATCATCCTCATTCTGGTGAACCTGGTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3494 ATGGCTTCACCTAGTGGCCCCAAGCATGACTTCTCCCATGTCAATGAGCACAGCCACATT 3553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3673 AAAGGCTATTTGCAGAAGGAGCTCACAGATCACATTGAAAGCATTGCATATTCAAACATC 3732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 aaaggatacttgcagaaggaggtgacagaccacatggtgagtttggcttgctcggacatc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ttogtgatgggcottotggggaacagcgccaccattogggtcacccaggtgctgcagaag 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l atggcttcacccagcctcccgggcagtgactgctcccaaatcattgatcacagtcatgtc 60
                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye; 99% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 189108 bases at least Q40
Consensus quality: 189309 bases at least Q30
Consensus quality: 189307 bases at least Q20
Insert size: 189376; sum-of-contigs
Insert size: 143853; 4.8% error; agarose-fp
Quality coverage: 7.80x in Q20 bases; sum-of-contigs Quality
coverage: 10.32x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL157394 189476 bp DNA HTG 06-JUN-2001
Homo sapiens chromosome 10 clone RP11-399019, *** SEQUENCING IN
PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: plasmid; L08752; 99% of reads sequencing vector: plasmid; L08752; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On May 20, 2001 this sequence version replaced gi:14132822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blakey,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL157394.14 GI:14161146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
                                               consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---- Genome Center
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FEATURES
                                                                                                                                                                                                                                                                                                                                                Db 169901 ATGGCTTCACCTAGTGGCCCCAAGCATGACTTCTCCCATGTCAATGAGCACAGCCACATT 169960
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                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                             Db 169961 CCCGAG-TTGAGGTGACCCCACGGTCCAGAATCATCCTCATTCTGGTGAACCTGGTTCTC 170019
                                                                                                                                                                                                                                                                                                    Ω
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                                                                                     Db 170080 AAAGGCTATTTGCAGAAGGAGCTCACAGATCACATTGAAAGCATTGCATATTCAAACATC 170139
                                                                                                                                                                          Db 170020 TTTGTGGTGGGCATACTGGGTAGGAGAATCACCCAAAGGTCACCCATGAGCTGCAGAAAA 170079
Db 170140 TIGGTCTTCTTTATTGGCATGCCCACAGGGTCTTCTGACCTCTGATTAGATC 170191
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                       241 ttggtgttcctcatcggcatgcccatggagttctacagcatcatctggaatc 292
                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 9.0%;
Local Similarity 66.1%;
hes 193; Conservative 0
                                                                                                                                                                                                                                                                                           61 cccgagtttgaggtggccacctggatcaaaaatcacccttattctggtgtacctgatcatc 120
                                                                                                                                                                                                                                                                                                                                                                           1 atggcttcacccagcctcccgggcagtgactgctcccaaatcattgatcacagtcatgtc 60
                                                                                                              aaaggatacttgcagaaggaggtgacagaccacatggtgagtttggcttgctcggacatc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56130 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 187313: contid of 187313 bp in length
187314 187413: gap of 100 bp
187414 189476: contid of 2063 bp in length.
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/note="assembly_fragment:02382"
<sub>1</sub> 36795 c 37273 g 59178 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector_side:left"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment:04006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP11-399019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .189476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .187313
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 123.2; DB 2; pred. No. 3.4e-15; 0; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                            98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 189476;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Search completed: January 8, 2002, 22:26:59